Applicants wish to draw the Examiner's attention to the protein sequence presented in Figure 1, "ID-30, Clone 38". Applicants request the Examiner's consideration of the proposed amendment of this figure, including the amendment of the recited protein sequence in ID-30, Clone 38. The nucleotide and protein sequences as set forth in Figure 1, ID-30, Clone 38 are represented in the substitute Sequence Listing by SEQ ID NOs: 55 and 56. However, an obviously incorrect protein sequence, not encoded by the nucleotide sequence of SEQ ID NO:55, was presented in Figure 1, ID-30, Clone 38 as originally filed. The correct protein sequence encoded by SEQ ID NO:55 is presented in the instant substitute Sequence Listing as SEQ ID NO:56. As originally filed, the specification contemplates "a number of full length nucleotide sequences encoding antigenic *Group B Streptococcus* proteins" as well as the "corresponding amino acid sequences" as set forth in Figure 1. *See* Specification, page 14, lines 1-2. Therefore, the proposed amendment to the protein sequence of Figure 1, ID-30, Clone 38 does not constitute new matter. Accordingly, Applicants assert that no new matter is introduced by way of the proposed amendments to Figure 1.

Applicants respectfully request consideration of the proposed amendments to the Figures and notification of acceptance of the Figure amendments by the Examiner.

Specification

Please amend the specification to recite the following replacement paragraphs. A marked-up version showing changes made to the specification through the replacement paragraphs is contained herewith.

Please replace the current paragraph located on page 23, lines 14-24, with the following replacement paragraph:

--All forward and reverse oligonucleotide primers incorporated appropriate restriction enzyme sites to facilitate cloning into the pcDNA3.1 MCS region. All forward primers were also designed to include the conserved Kozak nucleotide sequence 5'-gccacc-3' immediately upstream of an 'atg' translation initiation codon in frame with the target gene insert. The Kozak sequence facilitates the recognition of initiator sequences by eukaryotic ribosomes. Typically, a forward primer incorporating a BamH1 restriction enzyme site the primer would begin with the sequence 5'-cgggatccgccaccatg-3' (SEQ ID NO: 199), followed by a sequence homologous to the 5' end of that part of a gene being amplified. All reverse primers incorporated a Not I restriction enzyme site sequence 5'-ttgcggccgc-3' (SEQ ID NO:200).